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SEQUENCE LISTING

<110> Syrrx, Inc.

<120> HISTONE DEACETYLASE INHIBITORS

<130> SYR-HDAC-5005-C1

<140> US 10/803,575
<141> 2004-03-17

<150> US 60/455,437
<151> 2003-03-17

<150> US 60/531,203
<151> 2003-12-19

<160> 8

<170> PatentIn version 3.2

<210> 1
<211> 513
<212> PRT
<213> Artificial

<220>
<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 1

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Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1               5                  10                  15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
            20                  25                  30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
        35                  40                  45

Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
    50                  55                  60

Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
65                  70                  75                  80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
                85                  90                  95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
            100                 105                 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
        115                 120                 125
```

```
Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
    130                 135                 140

Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
145                 150                 155                 160

Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
                165                 170                 175

Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
            180                 185                 190

Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
        195                 200                 205

His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
    210                 215                 220

Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
225                 230                 235                 240

Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
                245                 250                 255

Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
            260                 265                 270

Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
        275                 280                 285

Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
    290                 295                 300

Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
305                 310                 315                 320

Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
                325                 330                 335

Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
            340                 345                 350

Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
        355                 360                 365

Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
    370                 375                 380
```

Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
500 505 510

Ala

<210> 2
<211> 1542
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-482 of HDAC1 with a "MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 2
atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg 60

tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg cacccggagg 120

aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca 180

atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240

aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300

gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag 360

cagatgcaga gattcaacgt tggtgaggac tgtccagtat tcgatggcct gtttgagttc 420

tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480

gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcatctggc 540

ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600

gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660

acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720

gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780

gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg 840

gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900

cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag 960

agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc 1020

cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080

tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat 1140

atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200

cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc 1260

cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc 1320

tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380

ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa 1440

gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500

ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga 1542

<210> 3
<211> 498
<212> PRT
<213> Artificial

<220>
<223> Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 3

Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
50 55 60

```
Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65                  70                  75                  80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
                85                  90                  95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
            100                 105                 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
        115                 120                 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
    130                 135                 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145                 150                 155                 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
                165                 170                 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
            180                 185                 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
        195                 200                 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
    210                 215                 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225                 230                 235                 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
                245                 250                 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
            260                 265                 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
        275                 280                 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
    290                 295                 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
```

305 310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
420 425 430

Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
435 440 445

Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
450 455 460

Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
465 470 475 480

Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
485 490 495

His His

<210> 4
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4
atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac 60

ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc 120

atgacccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc 180

cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta 240

cggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatgtt 300

ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt 360

tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct 420

ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt 480

gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat 540

attcatcatg gtgatggtgt tgaagaagct ttttatacaa cagatcgtgt aatgacggta 600

tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct 660

ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca 720

tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgct 780

gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta 840

acagtcaaag gtcatgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg 900

atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact 960

gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat 1020

tttggaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca 1080

gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca 1140

cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa 1200

gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt 1260

gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat 1320

cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa 1380

aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc 1440

aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcactaa 1497

<210> 5
<211> 782
<212> PRT
<213> Artificial

<220>
<223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 5

Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr
1 5 10 15

```
Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
            20                  25                  30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
        35                  40                  45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
    50                  55                  60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
65                  70                  75                  80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
                85                  90                  95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser
            100                 105                 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val
        115                 120                 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly
    130                 135                 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His
145                 150                 155                 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg
                165                 170                 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe
            180                 185                 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr
        195                 200                 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr
    210                 215                 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn
225                 230                 235                 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val
                245                 250                 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala
            260                 265                 270
```

```
Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
        275                 280                 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
    290                 295                 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305                 310                 315                 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
                325                 330                 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
            340                 345                 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
        355                 360                 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
    370                 375                 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385                 390                 395                 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
                405                 410                 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
            420                 425                 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
        435                 440                 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
    450                 455                 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465                 470                 475                 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
                485                 490                 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
            500                 505                 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
```

515 520 525

Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540

Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
545 550 555 560

Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
565 570 575

Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
580 585 590

Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr
595 600 605

Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620

Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640

Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655

Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670

Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685

Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700

Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720

Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735

Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750

Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

Val Glu Asp Arg Glu Gly Pro Gly His His His His His His
770 775 780

<210> 6
<211> 2349
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 6
atgcccggga tggatctgaa ccttgaggct gaagcactgg ctggcactgg cttggtgttg 60

gatgagcagt taaatgaatt ccattgcctc tgggatgaca gcttcccgga aggccctgag 120

cggctccatg ccatcaagga gcaactgatc caggagggcc tcctagatcg ctgcgtgtcc 180

tttcaggccc ggtttgctga aaaggaagag ctgatgttgg ttcacagcct agaatatatt 240

gatctgatgg aaacaaccca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300

tacgactcag tttatctgca tccgaactca tactcctgtg cctgcctggc ctcaggctct 360

gtcctcaggc tggtggatgc ggtcctgggg gctgagatcc ggaatggcat ggccatcatt 420

aggcctcctg gacatcacgc ccagcacagt cttatggatg gctattgcat gttcaaccac 480

gtggctgtgg cagcccgcta tgctcaacag aaacaccgca tccggagggt ccttatcgta 540

gattgggatg tgcaccacgg tcaaggaaca cagttcacct tcgaccagga ccccagtgtc 600

ctctatttct ccatccaccg ctacgagcag ggtaggttct ggccccacct gaaggcctct 660

aactggtcca ccacaggttt cggccaaggc caaggatata ccatcaatgt gccttggaac 720

caggtgggga tgcgggatgc tgactacatt gctgctttcc tgcacgtcct gctgccagtc 780

gccctcgagt tccagcctca gctggtcctg gtggctgctg gatttgatgc cctgcaaggg 840

gaccccaagg gtgagatggc cgccactccg gcagggttcg cccagctaac ccacctgctc 900

atgggtctgg caggaggcaa gctgatcctg tctctggagg gtggctacaa cctccgcgcc 960

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cttgagccct tctgggaggt tcttgtgaga tcaactgaga ccgtggagag ggacaacatg 1140

gaggaggaca atgtagagga gagcgaggag gaaggaccct gggagccccc tgtgctccca 1200

atcctgacat ggccagtgct acagtctcgc acagggctgg tctatgacca aaatatgatg 1260

aatcactgca acttgtggga cagccaccac cctgaggtac cccagcgcat cttgcggatc 1320

atgtgccgtc tggaggagct gggccttgcc gggcgctgcc tcaccctgac accgcgccct 1380

gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccgggcc 1440

acagagaaaa tgaaaacccg ggagctgcac cgtgagagtt ccaactttga ctccatctat 1500

atctgcccca gtaccttcgc ctgtgcacag cttgccactg gcgctgcctg ccgcctggtg 1560

gaggctgtgc tctcaggaga ggttctgaat ggtgctgctg tggtgcgtcc cccaggacac 1620

cacgcagagc aggatgcagc ttgcggtttt tgctttttca actctgtggc tgtggctgct 1680

cgccatgccc agactatcag tgggcatgcc ctacggatcc tgattgtgga ttgggatgtc 1740

caccacggta atggaactca gcacatgttt gaggatgacc ccagtgtgct atatgtgtcc 1800

ctgcaccgct atgatcatgg caccttcttc cccatggggg atgagggtgc cagcagccag 1860

atcggccggg ctgcgggcac aggcttcacc gtcaacgtgg catggaacgg gccccgcatg 1920

ggtgatgctg actacctagc tgcctggcat cgcctggtgc ttcccattgc ctacgagttt 1980

aacccagaac tggtgctggt ctcagctggc tttgatgctg cacgggggga tccgctgggg 2040

ggctgccagg tgtcacctga gggttatgcc cacctcaccc acctgctgat gggccttgcc 2100

agtggccgca ttatccttat cctagagggt ggctataacc tgacatccat ctcagagtcc 2160

atggctgcct gcactcgctc cctccttgga gacccaccac ccctgctgac cctgccacgg 2220

cccccactat caggggccct ggcctcaatc actgagacca tccaagtcca tcgcagatac 2280

tggcgcagct tacgggtcat gaaggtagaa gacagagaag gacccgggca tcaccatcac 2340

catcactaa 2349

<210> 7
<211> 385
<212> PRT
<213> Artificial

<220>
<223> Residues 1-377 of HDAC8 with a "MHHHHHHP" tag at the N-terminus

<400> 7

Met His His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala
1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp

85 90 95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
370 375 380

Val
385

<210> 8
<211> 1158
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 1-377 of HDAC8 with a "MHHHHHHP" tag at the N-terminus

<400> 8
atgcaccatc accatcacca tcccatggag gagccggagg aaccggcgga cagtgggcag 60

tcgctggtcc cggtttatat ctatagtccc gagtatgtca gtatgtgtga ctccctggcc 120

aagatcccca aacgggccag tatggtgcat tctttgattg aagcatatgc actgcataag 180

cagatgagga tagttaagcc taaagtggcc tccatggagg agatggccgc cttccacact 240

gatgcttatc tgcagcatct ccagaaggtc agccaagagg gcgatgatga tcatccggac 300

tccatagaat atgggctagg ttatgactgc ccagccactg aagggatatt tgactatgca 360

gcagctatag gaggggctac gatcacagct gcccaatgcc tgattgacgg aatgtgcaaa 420

gtagcaatta actggtctgg agggtggcat catgcaaaga aagatgaagc atctggtttt 480

tgttatctca atgatgctgt cctgggaata ttacgattgc gacggaaatt tgagcgtatt 540

ctctacgtgg atttggatct gcaccatgga gatggtgtag aagacgcatt cagtttcacc 600

tccaaagtca tgaccgtgtc cctgcacaaa ttctccccag gatttttccc aggaacaggt 660

gacgtgtctg atgttggcct agggaaggga cggtactaca gtgtaaatgt gcccattcag 720

gatggcatac aagatgaaaa atattaccag atctgtgaaa gtgtactaaa ggaagtatac 780

caagccttta atcccaaagc agtggtctta cagctgggag ctgacacaat agctggggat 840

cccatgtgct cctttaacat gactccagtg ggaattggca agtgtcttaa gtacatcctt 900

caatggcagt tggcaacact cattttggga ggaggaggct ataaccttgc caacacggct 960

cgatgctgga catacttgac cggggtcatc ctagggaaaa cactatcctc tgagatccca 1020

gatcatgagt ttttcacagc atatggtcct gattatgtgc tggaaatcac gccaagctgc 1080

cggccagacc gcaatgagcc ccaccgaatc caacaaatcc tcaactacat caaagggaat 1140

ctgaagcatg tggtctag 1158

SYR-HDAC-5005-C1 sub seq list 2.ST25
SEQUENCE LISTING

<110> Syrrx, Inc.

<120> HISTONE DEACETYLASE INHIBITORS

<130> SYR-HDAC-5005-C1

<140> US 10/803,575
<141> 2004-03-17

<150> US 60/455,437
<151> 2003-03-17

<150> US 60/531,203
<151> 2003-12-19

<160> 8

<170> PatentIn version 3.2

<210> 1
<211> 513
<212> PRT
<213> Artificial

<220>
<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 1

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
35 40 45

Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
50 55 60

Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
65 70 75 80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
115 120 125

```
Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
    130                 135                 140

Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
145                 150                 155                 160

Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
                165                 170                 175

Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
            180                 185                 190

Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
        195                 200                 205

His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
    210                 215                 220

Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
225                 230                 235                 240

Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
                245                 250                 255

Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
            260                 265                 270

Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
        275                 280                 285

Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
    290                 295                 300

Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
305                 310                 315                 320

Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
                325                 330                 335

Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
            340                 345                 350

Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
        355                 360                 365

Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
    370                 375                 380
```

Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
500 505 510

Ala

<210> 2
<211> 1542
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-482 of HDAC1 with a "MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 2
atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg 60

tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg cacccggagg 120

aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca 180

atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240

aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300

gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag 360

cagatgcaga gattcaacgt tggtgaggac tgtccagtat tcgatggcct gtttgagttc 420

tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480

gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcatctggc 540

ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600

gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660

acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720

gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780

gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg 840

gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900

cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag 960

agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc 1020

cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080

tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat 1140

atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200

cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc 1260

cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc 1320

tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380

ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa 1440

gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500

ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga 1542

<210> 3
<211> 498
<212> PRT
<213> Artificial

<220>
<223> Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 3

Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
50 55 60

Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr

305 310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
420 425 430

Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
435 440 445

Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
450 455 460

Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
465 470 475 480

Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
485 490 495

His His

<210> 4
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4
atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac 60

ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc 120

atgacccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc 180

cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta 240

cggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatgtt 300

ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt 360

tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct 420

ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt 480

gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat 540

attcatcatg gtgatggtgt tgaagaagct ttttatacaa cagatcgtgt aatgacggta 600

tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct 660

ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca 720

tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgct 780

gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta 840

acagtcaaag gtcatgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg 900

atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact 960

gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat 1020

tttggaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca 1080

gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca 1140

cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa 1200

gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt 1260

gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat 1320

cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa 1380

aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc 1440

aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcactaa 1497

<210> 5
<211> 782
<212> PRT
<213> Artificial

<220>
<223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 5

Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr
1 5 10 15

```
Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
            20                  25                  30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
        35                  40                  45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
    50                  55                  60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
65                  70                  75                  80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
                85                  90                  95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser
            100                 105                 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val
        115                 120                 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly
    130                 135                 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His
145                 150                 155                 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg
                165                 170                 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe
            180                 185                 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr
        195                 200                 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr
    210                 215                 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn
225                 230                 235                 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val
                245                 250                 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala
            260                 265                 270
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```
Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
        275                 280                 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
    290                 295                 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305                 310                 315                 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
                325                 330                 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
            340                 345                 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
        355                 360                 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
    370                 375                 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385                 390                 395                 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
                405                 410                 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
            420                 425                 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
        435                 440                 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
    450                 455                 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465                 470                 475                 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
                485                 490                 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
            500                 505                 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
```

515 520 525

Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540

Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
545 550 555 560

Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
565 570 575

Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
580 585 590

Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr
595 600 605

Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620

Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640

Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655

Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670

Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685

Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700

Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720

Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735

Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750

Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

Val Glu Asp Arg Glu Gly Pro Gly His His His His His His
770 775 780

<210> 6
<211> 2349
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 6
atgcccggga tggatctgaa ccttgaggct gaagcactgg ctggcactgg cttggtgttg 60

gatgagcagt taaatgaatt ccattgcctc tgggatgaca gcttcccgga aggccctgag 120

cggctccatg ccatcaagga gcaactgatc caggagggcc tcctagatcg ctgcgtgtcc 180

tttcaggccc ggtttgctga aaaggaagag ctgatgttgg ttcacagcct agaatatatt 240

gatctgatgg aaacaaccca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300

tacgactcag tttatctgca tccgaactca tactcctgtg cctgcctggc ctcaggctct 360

gtcctcaggc tggtggatgc ggtcctgggg gctgagatcc ggaatggcat ggccatcatt 420

aggcctcctg gacatcacgc ccagcacagt cttatggatg gctattgcat gttcaaccac 480

gtggctgtgg cagcccgcta tgctcaacag aaacaccgca tccggagggt ccttatcgta 540

gattgggatg tgcaccacgg tcaaggaaca cagttcacct tcgaccagga ccccagtgtc 600

ctctatttct ccatccaccg ctacgagcag ggtaggttct ggccccacct gaaggcctct 660

aactggtcca ccacaggttt cggccaaggc caaggatata ccatcaatgt gccttggaac 720

caggtgggga tgcgggatgc tgactacatt gctgctttcc tgcacgtcct gctgccagtc 780

gccctcgagt tccagcctca gctggtcctg gtggctgctg gatttgatgc cctgcaaggg 840

gaccccaagg gtgagatggc cgccactccg gcagggttcg cccagctaac ccacctgctc 900

atgggtctgg caggaggcaa gctgatcctg tctctggagg gtggctacaa cctccgcgcc 960

ctggctgaag gcgtcagtgc ttcgctccac acccttctgg gagacccttg ccccatgctg 1020

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cttgagccct tctgggaggt tcttgtgaga tcaactgaga ccgtggagag ggacaacatg 1140

gaggaggaca atgtagagga gagcgaggag gaaggaccct gggagccccc tgtgctccca 1200

atcctgacat ggccagtgct acagtctcgc acagggctgg tctatgacca aaatatgatg 1260

aatcactgca acttgtggga cagccaccac cctgaggtac cccagcgcat cttgcggatc 1320

atgtgccgtc tggaggagct gggccttgcc gggcgctgcc tcaccctgac accgcgccct 1380

gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccgggcc 1440

acagagaaaa tgaaaacccg ggagctgcac cgtgagagtt ccaactttga ctccatctat 1500

atctgcccca gtaccttcgc ctgtgcacag cttgccactg gcgctgcctg ccgcctggtg 1560

gaggctgtgc tctcaggaga ggttctgaat ggtgctgctg tggtgcgtcc cccaggacac 1620

cacgcagagc aggatgcagc ttgcggtttt tgctttttca actctgtggc tgtggctgct 1680

cgccatgccc agactatcag tgggcatgcc ctacggatcc tgattgtgga ttgggatgtc 1740

caccacggta atggaactca gcacatgttt gaggatgacc ccagtgtgct atatgtgtcc 1800

ctgcaccgct atgatcatgg caccttcttc cccatggggg atgagggtgc cagcagccag 1860

atcggccggg ctgcgggcac aggcttcacc gtcaacgtgg catggaacgg gccccgcatg 1920

ggtgatgctg actacctagc tgcctggcat cgcctggtgc ttcccattgc ctacgagttt 1980

aacccagaac tggtgctggt ctcagctggc tttgatgctg cacgggggga tccgctgggg 2040

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agtggccgca ttatccttat cctagagggt ggctataacc tgacatccat ctcagagtcc 2160

atggctgcct gcactcgctc cctccttgga gacccaccac ccctgctgac cctgccacgg 2220

cccccactat caggggccct ggcctcaatc actgagacca tccaagtcca tcgcagatac 2280

tggcgcagct tacgggtcat gaaggtagaa gacagagaag gacccgggca tcaccatcac 2340

catcactaa 2349

<210> 7
<211> 385
<212> PRT
<213> Artificial

<220>
<223> Residues 1-377 of HDAC8 with a "MHHHHHHP" tag at the N-terminus

<400> 7

Met His His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala
1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp

85 90 95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
370 375 380

Val
385

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<211> 1158
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 1-377 of HDAC8 with a "MHHHHHHP" tag at the N-terminus

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aagatcccca aacgggccag tatggtgcat tctttgattg aagcatatgc actgcataag 180

cagatgagga tagttaagcc taaagtggcc tccatggagg agatggccgc cttccacact 240

gatgcttatc tgcagcatct ccagaaggtc agccaagagg gcgatgatga tcatccggac 300

tccatagaat atgggctagg ttatgactgc ccagccactg aagggatatt tgactatgca 360

gcagctatag gaggggctac gatcacagct gcccaatgcc tgattgacgg aatgtgcaaa 420

gtagcaatta actggtctgg agggtggcat catgcaaaga aagatgaagc atctggtttt 480

tgttatctca atgatgctgt cctgggaata ttacgattgc gacggaaatt tgagcgtatt 540

ctctacgtgg atttggatct gcaccatgga gatggtgtag aagacgcatt cagtttcacc 600

tccaaagtca tgaccgtgtc cctgcacaaa ttctccccag gatttttccc aggaacaggt 660

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cccatgtgct cctttaacat gactccagtg ggaattggca agtgtcttaa gtacatcctt 900

caatggcagt tggcaacact cattttggga ggaggaggct ataaccttgc caacacggct 960

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